



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/807,096

Source:

FWO-

Date Processed by STIC:

3/30/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/807,096

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2        Invalid Line Length    The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3        Misaligned Amino    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4        Non-ASCII    The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5        Variable Length    Sequence(s)        contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6        PatentIn 2.0    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7        Skipped Sequences    Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence:  
(OLD RULES)    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                  (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                  This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8        Skipped Sequences    Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence.  
(NEW RULES)    <210> sequence id number  
                  <400> sequence id number  
                  000
- 9        Use of n's or Xaa's    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10        Invalid <213>    Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
Response    scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11        Use of <220>    Sequence(s)        missing the <220> "Feature" and associated numeric identifiers and responses.  
                  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                  (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12        PatentIn 2.0    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
"bug"    resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13        Misuse of n/Xaa    "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

DATE: 03/30/2004

PATENT APPLICATION: US/10/807,096

TIME: 13:11:07

Input Set : A:\01-SQ Listing-22 Mar 2004.txt

Output Set: N:\CRF4\03302004\J807096.raw

3 &lt;110&gt; APPLICANT: Svendsen, Allan

4 Minning, Stefan

6 &lt;120&gt; TITLE OF INVENTION: Subtilases

8 &lt;130&gt; FILE REFERENCE: 10321.200-US

C--&gt; 10 &lt;140&gt; CURRENT APPLICATION NUMBER: US/10/807,096

C--&gt; 10 &lt;141&gt; CURRENT FILING DATE: 2004-03-22

E--&gt; 10 &lt;160&gt; NUMBER OF SEQ ID NOS: 11

12 &lt;170&gt; SOFTWARE: PatentIn version 3.2

Found 7

## ERRORED SEQUENCES

510 &lt;210&gt; SEQ ID NO: 7

511 &lt;211&gt; LENGTH: 311

512 &lt;212&gt; TYPE: PRT

513 &lt;213&gt; ORGANISM: Bacillus sp. TY145

516 &lt;220&gt; FEATURE:

517 &lt;221&gt; NAME/KEY: peptide

518 &lt;222&gt; LOCATION: (1)..(311)

520 &lt;400&gt; SEQUENCE: 7

522 Ala Val Pro Ser Thr Gln Thr Pro Trp Gly Ile Lys Ser Ile Tyr Asn

523 1 5 10 15

526 Asp Gln Ser Ile Thr Lys Thr Thr Gly Gly Ser Gly Ile Lys Val Ala

527 20 25 30

530 Val Leu Asp Thr Gly Val Tyr Thr Ser His Leu Asp Leu Ala Gly Ser

531 35 40 45

534 Ala Glu Gln Cys Lys Asp Phe Thr Gln Ser Asn Pro Leu Val Asp Gly

535 50 55 60

538 Ser Cys Thr Asp Arg Gln Gly His Gly Thr His Val Ala Gly Thr Val

539 65 70 75 80

542 Leu Ala His Gly Gly Ser Asn Gly Gln Gly Val Tyr Gly Val Ala Pro

543 85 90 95

546 Gln Ala Lys Leu Trp Ala Tyr Lys Val Leu Gly Asp Asn Gly Ser Gly

547 100 105 110

550 Tyr Ser Asp Asp Ile Ala Ala Ala Ile Arg His Val Ala Asp Glu Ala

551 115 120 125

554 Ser Arg Thr Gly Ser Lys Val Val Ile Asn Met Ser Leu Gly Ser Ser

555 130 135 140

558 Ala Lys Asp Ser Leu Ile Ala Ser Ala Val Asp Tyr Ala Tyr Gly Lys

559 145 150 155 160

562 Gly Val Leu Ile Val Ala Ala Ala Gly Asn Ser Gly Ser Gly Ser Asn

563 165 170 175

566 Thr Ile Gly Phe Pro Gly Gly Leu Val Asn Ala Val Ala Val Ala Ala

Does Not Comply  
Corrected Diskette Needed

(pg. 1-4)

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/807,096

DATE: 03/30/2004

TIME: 13:11:07

Input Set : A:\01-SQ Listing-22 Mar 2004.txt

Output Set: N:\CRF4\03302004\J807096.raw

567				180				185					190				
570	Leu	Glu	Asn	Val	Gln	Gln	Asn	Gly	Thr	Tyr	Arg	Val	Ala	Asp	Phe	Ser	
571				195				200					205				
574	Ser	Arg	Gly	Asn	Pro	Ala	Thr	Ala	Gly	Asp	Tyr	Ile	Ile	Gln	Glu	Arg	
575		210					215					220					
578	Asp	Ile	Glu	Val	Ser	Ala	Pro	Gly	Ala	Ser	Val	Glu	Ser	Thr	Trp	Tyr	
579	225					230					235					240	
582	Thr	Gly	Gly	Tyr	Asn	Thr	Ile	Ser	Gly	Thr	Ser	Met	Ala	Thr	Pro	His	
583					245					250						255	
586	Val	Ala	Gly	Leu	Ala	Ala	Lys	Ile	Trp	Ser	Ala	Asn	Thr	Ser	Leu	Ser	
587				260					265					270			
590	His	Ser	Gln	Leu	Arg	Thr	Glu	Leu	Gln	Asn	Arg	Ala	Lys	Val	Tyr	Asp	
591			275					280					285				
594	Ile	Lys	Gly	Gly	Ile	Gly	Ala	Gly	Thr	Gly	Asp	Asp	Tyr	Ala	Ser	Gly	
595		290					295					300					
598	Phe	Gly	Tyr	Pro	Arg	Val	Lys										
599	305					310											

E--&gt; 605 1



## VERIFICATION SUMMARY

DATE: 03/30/2004

PATENT APPLICATION: US/10/807,096

TIME: 13:11:08

Input Set : A:\01-SQ Listing-22 Mar 2004.txt

Output Set: N:\CRF4\03302004\J807096.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:605 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7

L:10 M:203 E: No. of Seq. differs, &lt;160&gt; Number Of Sequences:Input (11) Counted (7)

<210> 5  
<211> 7  
<212> PRT  
<213> Partiel sequence

-Invalid Response

Mandatory, <213>

Response has to be either  
Artificial/Unknown

on Genus/Species.

<220>  
<221> peptide  
<222> (1)..(7)

<400> 5

Leu Asn Asn Ser Ile Gly Val  
1 5

<210> 6  
<211> 3  
<212> PRT  
<213> Partiel sequence

-Invalid Response

<220>  
<221> peptide  
<222> (1)..(3)

<400> 6

Ser Ser Asn  
1

Please see item # 10  
ON error summary  
sheet.